

Caspian tiger phylogeography

The extinct Caspian tiger (*Panthera tigris virgata*, Illiger, 1815) recently inhabited Central Asian forest and riverine systems from Xinjiang to Anatolia in a range seemingly disjunct from that of other tigers. The Caspian tiger's obscure biogeographical origin and uncertain phylogenetic placement in the tiger family tree has puzzled naturalists for over a century, while surviving tiger subspecies are a major conservation priority. Here we use ancient-DNA methodologies to generate a composite 1257 bp mtDNA haplotype from twenty wild-caught Caspian tigers sampled across their historical range to resolve these issues. Caspian tigers carry a major mtDNA haplotype that differs by a single residue from the monomorphic haplotype found in contemporary Amur (Siberian) tigers (*P. t. altaica*). A phylogeographical analysis of *P. t. virgata* in the context of the five living tiger subspecies provides evidence for a Caspian tiger colonization of Central Asia less than 10,000 years ago via a westerly migration through the narrow Gansu Corridor (Silk Road), followed by a more recent easterly return across northern Asia to establish the Amur tiger population living today in the Russian Far East. The severe genetic depletion characteristic of Amur tigers today likely reflects these founder migrations, predating any anthropogenic influence. Due to their recent propinquity, living Amur tigers (wild and captive) would provide a plausible genetic reservoir upon which to draw should tiger reintroductions to the former range of the Caspian tiger be implemented.

A Near Eastern Origin of Cat Domestication

The domestic cat is the world's most popular pet, numbering more than 600 million and is also an important medical model for genetic diseases, yet little is known with certainty of the cat's origin, early natural history or genetic background. To investigate the relationships between domestic cats and their indigenous wild congeners we typed 36 short tandem repeat loci and sequenced 2.6 kb of the mitochondrial genes ND5 and ND6 in ~1000 cats from wild and domestic settings, including representatives of registered-breed and random-bred pet cats from both feral and household environments. Additionally, six *Felis bieti* and twelve *F. margarita*, the closest relatives of *F. silvestris*, were included as comparative outgroups. Phylogenetic and clustering analyses identified five genetically distinctive wildcat populations, present in Europe (*F.s. silvestris*), Southern Africa (*F.s. caffra*), Central Asia (*F.s. ornata*), the Near East (*F.s. lybica*) and China (*F.s. bieti*), here subsumed under *F. silvestris*. Domestic cats carried genetic signatures that differentiated them from all wildcats, including the critically endangered Scottish wildcat, except those from the Near East. Multiple genetic analyses produced concordant results tracing the origins of cat domestication to at least five maternal wildcat lines originating in the Near East.